

Pleaseconsult  
sequenceRules for Valid format

1600

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/487,790DATE: 10/18/2002  
TIME: 10:12:02Input Set : A:\EP.txt  
Output Set: N:\CRF4\10182002\I487790.raw**Does Not Comply  
Corrected Diskette Needed**

## SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:  
 4 (i) APPLICANT: HADASIT MEDICAL RESEARCH SERVICES AND DEVELOPMENT COMPANY  
 5 LTD.  
 6 (ii) TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES  
 7 (iii) NUMBER OF SEQUENCES: 12  
 C--> 9 (vi) CURRENT APPLICATION DATA:  
 C--> 10 (A) APPLICATION NUMBER: US/09/487,790  
 C--> 11 (B) FILING DATE: 20-Jan-2000  
 12 (C) CLASSIFICATION:  
 13 (vii) PRIOR APPLICATION DATA:  
 14 (A) APPLICATION NUMBER:  
 15 (B) FILING DATE:

see pp 1-3

(v) CORRESPONDENCE ADDRESS:  
 (A) ADDRESSEE:  
 (B) STREET:  
 (C) CITY:  
 (D) STATE:  
 (E) COUNTRY:  
 (F) ZIP:  
 (M) COMPUTER READABLE FORM:  
 (A) MEDIUM TYPE:  
 (B) COMPUTER:  
 (C) OPERATING SYSTEM:  
 (D) SOFTWARE:

## ERRORED SEQUENCES

E--> 17 (2) INFORMATION FOR SEQ ID NO: 1:  
 18 (i) SEQUENCE CHARACTERISTICS:  
 19 (A) LENGTH: 21  
 20 (B) TYPE: amino acid  
 21 (C) STRANDEDNESS: single  
 22 (D) TOPOLOGY: linear  
 E--> 23 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 24 Lys Gly Ser Trp Tyr Ser Met Arg Lys Met Ser Met Lys Ile Arg Pro Phe Phe Pro,  
 E--> 25 Glu Glu  
 26 (2) INFORMATION FOR SEQ ID NO: 2:  
 27 (i) SEQUENCE CHARACTERISTICS:  
 28 (A) LENGTH: 21  
 29 (B) TYPE: amino acid  
 30 (C) STRANDEDNESS: single  
 31 (D) TOPOLOGY: linear  
 32 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 E--> 33 Lys Thr Arg Trp Tyr Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn Arg  
 E--> 34 Leu Thr  
 35 (2) INFORMATION FOR SEQ ID NO: 3:  
 36 (i) SEQUENCE CHARACTERISTICS:  
 37 (A) LENGTH: 20  
 38 (B) TYPE: amino acid  
 39 (C) STRANDEDNESS: single  
 40 (D) TOPOLOGY: linear  
 41 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 E--> 42 Arg Gly Ala Asp Tyr Ser Leu Arg Ala Val Arg Met Lys Ile Arg Pro Leu Val Thr

use the "not letter 'l'  
numeral '1' 1insert  
these  
mandatory  
headers  
and responses  
for a U.S.  
applicationPer Sequence Rules  
A maximum of 16  
amino acids per  
lineinsert  
hard  
returnnumber the  
amino acids  
under every 5 amino acids  
(GLOBAL ERROR) (see Error  
summary sheet)do not use numeral '1'  
same errors as aboveinvalid  
Ile?FYI: all U.S.  
applications which  
do not have a  
prior application  
filed before  
July 1, 1998,  
need to  
be in  
"new"  
Sequence  
Rules  
format

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RECEIVED

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OCT 25 2002

TECH CENTER 1600/2900

E--> 43 Glu

53 (2) INFORMATION FOR SEQ ID NO: 5:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 20

56 (B) TYPE: amino acid

57 (C) STRANDEDNESS: single

58 (D) TOPOLOGY: linear

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

E--> 60 Leu Thr lle Gly Glu Gly Glu Glu His His Leu Gly Gly Ala Lys Glu Ala Gly Asp

E--> 61 Val

C--> 62 (2) INFORMATION FOR SEQ ID NO: 6:

63 (i) SEQUENCE CHARACTERISTICS:

64 (A) LENGTH: 29

65 (B) TYPE: amino acid

66 (C) STRANDEDNESS: single

67 (D) TOPOLOGY: linear

68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

E--> 69 X X Gly Val Val Trp X X X X Gly X X Tyr Ser X Arg X X X Met Ly Invalid

E--> 70 lle Arg Pro X X X Glu

72 (2) INFORMATION FOR SEQ ID NO: 7:

73 (i) SEQUENCE CHARACTERISTICS:

74 (A) LENGTH: 65

75 (B) TYPE: nucleic acid

76 (C) STRANDEDNESS: double

77 (D) TOPOLOGY: linear

78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

E--> 79 AAGGGGTCATGGTATCAATGAGGAAGATGAGTATGAAGATCAGGCCCTTCTTCCCACAGCAATAG

81 (2) INFORMATION FOR SEQ ID NO: 8:

82 (i) SEQUENCE CHARACTERISTICS:

83 (A) LENGTH: 63

84 (B) TYPE: nucleic acid

85 (C) STRANDEDNESS: double

86 (D) TOPOLOGY: linear

87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

E--> 88 AGAGGGGCAGATTATTCCTCAGGGCTGTTGCGATGAAAATTAGGCCCTTGTGACCCAATAG

90 (2) INFORMATION FOR SEQ ID NO: 9:

91 (i) SEQUENCE CHARACTERISTICS:

92 (A) LENGTH: 63

93 (B) TYPE: nucleic acid

94 (C) STRANDEDNESS: double

95 (D) TOPOLOGY: linear

96 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

E--> 97 AAAACCCGGTGGTATTCATGAAGAAAACCACTATGAAGATAATCCATTCAACAGACTCACA

99 (2) INFORMATION FOR SEQ ID NO: 10:

100 (i) SEQUENCE CHARACTERISTICS:

101 (A) LENGTH: 15

102 (B) TYPE: amino acid

103 (C) STRANDEDNESS: single

104 (D) TOPOLOGY: linear

*same error*

*same error*

*one space between amino acids*

*do you mean Xaa? "X" is invalid*

*invalid. Per*

*Sequence*

*Rules,*

*group all non-coding*

*nucleotides*

*into 10's,*

*with a (one)*

*space*

*between*

*each*

*group*

*same error*

*same*

*Insert cumulative base total at right margin of each line*

*use numeral "0"  
NOT letter "O"*

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*same errors on previous pages*

105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10 *Ile? same error*

E--> 106 Tyr Ser (X) Arg (X X) Met Lys (Ile) Arg Pro (X X X) Glu *use Xaa*

C--> 108 (2) INFORMATION FOR SEQ ID NO: 11 *use numbers, not letters*

109 (i) SEQUENCE CHARACTERISTICS:

110 (A) LENGTH: 20 *insert*

111 (B) TYPE: amino acid

112 (C) STRANDEDNESS: single

113 (D) TOPOLOGY: linear

E--> 114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 *same error*

E--> 115 Lys (X X) Trp Tyr Ser Met (X) Lys (X X) Met Lys (Ile) (X) Pro Phe (X X X) *same error*

E--> 117 (2) INFORMATION FOR SEQ ID NO: 12 *Colon*

118 (i) SEQUENCE CHARACTERISTICS:

119 (A) LENGTH: 30 *use Ile?*

120 (B) TYPE: amino acid *number*

121 (C) STRANDEDNESS: single *"1"*

122 (D) TOPOLOGY: linear *use number "1" same*

E--> 123 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

E--> 124 Asp (X) Gly (X X) Trp (X X) Trp Lys (X X) Trp Tyr Ser Met (X) Lys (X X) Met Lys Ile (X)

E--> 125 Pro Phe (X X X X)

E--> 130 (1) *delete*

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/487,790

DATE: 10/18/2002  
TIME: 10:12:03

Input Set : A:\EP.txt  
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:6; Line(s) 69

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/487,790

DATE: 10/18/2002

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Input Set : A:\EP.txt

Output Set: N:\CRF4\10182002\I487790.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
 L:9 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]  
 L:9 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]  
 L:10 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
 L:11 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
 L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(B) STREET:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(C) CITY:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(D) STATE:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(E) COUNTRY:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(F) ZIP:] of (1)(iv)  
 L:17 M:202 E: (16) Value must be an Integer, Data=[1:]  
 L:23 M:212 E: (34) Invalid or duplicate Sequence ID Number, Value=[1:]  
 L:25 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0  
 L:33 M:330 E: (2) Invalid Amino Acid Designator, 2  
 L:34 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0  
 L:42 M:330 E: (2) Invalid Amino Acid Designator, 1  
 L:43 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0  
 L:60 M:330 E: (2) Invalid Amino Acid Designator, 1  
 L:61 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0  
 L:62 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]  
 L:69 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:69 M:330 E: (2) Invalid Amino Acid Designator, 13  
 L:70 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0  
 L:70 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:70 M:330 E: (2) Invalid Amino Acid Designator, 3  
 L:79 M:254 E: No. of Bases conflict, Input:0 Counted:65 SEQ:7  
 L:88 M:254 E: No. of Bases conflict, Input:0 Counted:63 SEQ:8  
 L:97 M:254 E: No. of Bases conflict, Input:0 Counted:63 SEQ:9  
 L:106 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:106 M:330 E: (2) Invalid Amino Acid Designator, 7  
 L:108 M:202 E: (16) Value must be an Integer, Data=[11]  
 L:108 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]  
 L:114 M:202 E: (16) Value must be an Integer, Data=[11:]  
 L:115 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:115 M:330 E: (2) Invalid Amino Acid Designator, 10  
 L:117 M:202 E: (16) Value must be an Integer, Data=[12]  
 L:123 M:202 E: (16) Value must be an Integer, Data=[12]  
 L:124 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:124 M:330 E: (2) Invalid Amino Acid Designator, 11  
 L:125 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0  
 L:125 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:125 M:330 E: (2) Invalid Amino Acid Designator, 4  
 M:332 Repeated in SeqNo=-1

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

09/487,790

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

Please  
Note